

Re-run

5050 WA



#5108 PCT

9/14/02

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,877

DATE: 05/08/2002

TIME: 11:03:35

Input Set : N:\paola\US09869877.raw

Output Set: N:\CRF3\05082002\I869877.raw

ENTERED

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1 <110> APPLICANT: Schneider, Palle
2   Danielsen, Steffen
3   Svendsen, Allan
4 <120> TITLE OF INVENTION: Laccase Mutants
5 <130> FILE REFERENCE: 10179.204-US
6 <140> CURRENT APPLICATION NUMBER: US/09/869,877
7 <141> CURRENT FILING DATE: 2001-07-06
8 <160> NUMBER OF SEQ ID NOS: 10
9 <170> SOFTWARE: PatentIn version 3.1
11 <210> SEQ ID NO: 1
12 <211> LENGTH: 539
13 <212> TYPE: PRT
14 <213> ORGANISM: Coprinus cinereus
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17   1             5             10             15
18   Asn Ala Gln Ile Val Asn Ser Val Asp Thr Met Thr Leu Thr Asn Ala
19   20             25             30
20   Asn Val Ser Pro Asp Gly Phe Thr Arg Ala Gly Ile Leu Val Asn Gly
21   35             40             45
22   Val His Gly Pro Leu Ile Arg Gly Gly Lys Asn Asp Asn Phe Glu Leu
23   50             55             60
24   Asn Val Val Asn Asp Leu Asp Asn Pro Thr Met Leu Arg Pro Thr Ser
25   65             70             75             80
26   Ile His Trp His Gly Leu Phe Gln Arg Gly Thr Asn Trp Ala Asp Gly
27   85             90             95
28   Ala Asp Gly Val Asn Gln Cys Pro Ile Ser Pro Gly His Ala Phe Leu
29   100            105            110
30   Tyr Lys Phe Thr Pro Ala Gly His Ala Gly Thr Phe Trp Tyr His Ser
31   115            120            125
32   His Phe Gly Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Met Val Ile
33   130            135            140
34   Tyr Asp Asp Asn Asp Pro His Ala Ala Leu Tyr Asp Glu Asp Asp Glu
35   145            150            155            160
36   Asn Thr Ile Ile Thr Leu Ala Asp Trp Tyr His Ile Pro Ala Pro Ser
37   165            170            175
38   Ile Gln Gly Ala Ala Gln Pro Asp Ala Thr Leu Ile Asn Gly Lys Gly
39   180            185            190
40   Arg Tyr Val Gly Gly Pro Ala Ala Glu Leu Ser Ile Val Asn Val Glu
41   195            200            205
42   Gln Gly Lys Lys Tyr Arg Met Arg Leu Ile Ser Leu Ser Cys Asp Pro
43   210            215            220
44   Asn Trp Gln Phe Ser Ile Asp Gly His Glu Leu Thr Ile Ile Glu Val

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45      225      230      235      240
46      Asp Gly Gln Leu Thr Glu Pro His Thr Val Asp Arg Leu Gln Ile Phe
47      245      250      255
48      Thr Gly Gln Arg Tyr Ser Phe Val Leu Asp Ala Asn Gln Pro Val Asp
49      260      265      270
50      Asn Tyr Trp Ile Arg Ala Gln Pro Asn Lys Gly Arg Asn Gly Leu Ala
51      275      280      285
52      Gly Thr Phe Ala Asn Gly Val Asn Ser Ala Ile Leu Arg Tyr Ala Gly
53      290      295      300
54      Ala Ala Asn Ala Asp Pro Thr Thr Ser Ala Asn Pro Asn Pro Ala Gln
55      305      310      315      320
56      Leu Asn Glu Ala Asp Leu His Ala Leu Ile Asp Pro Ala Ala Pro Gly
57      325      330      335
58      Ile Pro Thr Pro Gly Ala Ala Asp Val Asn Leu Arg Phe Gln Leu Gly
59      340      345      350
60      Phe Ser Gly Gly Arg Phe Thr Ile Asn Gly Thr Ala Tyr Glu Ser Pro
61      355      360      365
62      Ser Val Pro Thr Leu Leu Gln Ile Met Ser Gly Ala Gln Ser Ala Asn
63      370      375      380
64      Asp Leu Leu Pro Ala Gly Ser Val Tyr Glu Leu Pro Arg Asn Gln Val
65      385      390      395      400
66      Val Glu Leu Val Val Pro Ala Gly Val Leu Gly Gly Pro His Pro Phe
67      405      410      415
68      His Leu His Gly His Ala Phe Ser Val Val Arg Ser Ala Gly Ser Ser
69      420      425      430
70      Thr Tyr Asn Phe Val Asn Pro Val Lys Arg Asp Val Val Ser Leu Gly
71      435      440      445
72      Val Thr Gly Asp Glu Val Thr Ile Arg Phe Val Thr Asp Asn Pro Gly
73      450      455      460
74      Pro Trp Phe Phe His Cys His Ile Glu Phe His Leu Met Asn Gly Leu
75      465      470      475      480
76      Ala Ile Val Phe Ala Glu Asp Met Ala Asn Thr Val Asp Ala Asn Asn
77      485      490      495
78      Pro Pro Val Glu Trp Ala Gln Leu Cys Glu Ile Tyr Asp Asp Leu Pro
79      500      505      510
80      Pro Glu Ala Thr Ser Ile Gln Thr Val Val Arg Arg Ala Glu Pro Thr
81      515      520      525
82      Gly Phe Ser Ala Lys Phe Arg Arg Glu Gly Leu
83      530      535
85 <210> SEQ ID NO: 2
86 <211> LENGTH: 499
87 <212> TYPE: PRT
88 <213> ORGANISM: Polyporus pinsitus
89 <400> SEQUENCE: 2
90      Gly Ile Gly Pro Val Ala Asp Leu Thr Ile Thr Asn Ala Ala Val Ser
91      1      5      10      15
92      Pro Asp Gly Phe Ser Arg Gln Ala Val Val Val Asn Gly Gly Thr Pro
93      20      25      30
94      Gly Pro Leu Ile Thr Gly Asn Met Gly Asp Arg Phe Gln Leu Asn Val

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95																	
96	Ile	Asp	Asn	Leu	Thr	Asn	His	Thr	Met	Leu	Lys	Ser	Thr	Ser	Ile	His	
97		50					55					60					
98	Trp	His	Gly	Phe	Phe	Gln	Lys	Gly	Thr	Asn	Trp	Ala	Asp	Gly	Pro	Ala	
99	65					70				75					80		
100	Phe	Ile	Asn	Gln	Cys	Pro	Ile	Ser	Ser	Gly	His	Ser	Phe	Leu	Tyr	Asp	
101					85					90					95		
102	Phe	Gln	Val	Pro	Asp	Gln	Ala	Gly	Thr	Phe	Trp	Tyr	His	Ser	His	Leu	
103				100					105					110			
104	Ser	Thr	Gln	Tyr	Cys	Asp	Gly	Leu	Arg	Gly	Pro	Phe	Val	Val	Tyr	Asp	
105			115					120					125				
106	Pro	Asn	Asp	Pro	Ala	Ala	Asp	Leu	Tyr	Asp	Val	Asp	Asn	Asp	Asp	Thr	
107		130					135					140					
108	Val	Ile	Thr	Leu	Val	Asp	Trp	Tyr	His	Val	Ala	Lys	Leu	Gly	Pro		
109	145					150					155				160		
110	Ala	Phe	Pro	Leu	Gly	Ala	Asp	Ala	Thr	Leu	Ile	Asn	Gly	Lys	Gly	Arg	
111					165					170					175		
112	Ser	Pro	Ser	Thr	Thr	Thr	Ala	Asp	Leu	Ser	Val	Ile	Ser	Val	Thr	Pro	
113				180					185					190			
114	Gly	Lys	Arg	Tyr	Arg	Phe	Arg	Leu	Val	Ser	Leu	Ser	Cys	Asp	Pro	Asn	
115			195					200					205				
116	Tyr	Thr	Phe	Ser	Ile	Asp	Gly	His	Asn	Met	Thr	Ile	Ile	Glu	Thr	Asp	
117		210					215					220					
118	Ser	Ile	Asn	Thr	Ala	Pro	Leu	Val	Val	Asp	Ser	Ile	Gln	Ile	Phe	Ala	
119	225					230					235					240	
120	Ala	Gln	Arg	Tyr	Ser	Phe	Val	Leu	Glu	Ala	Asn	Gln	Ala	Val	Asp	Asn	
121					245					250					255		
122	Tyr	Trp	Ile	Arg	Ala	Asn	Pro	Asn	Phe	Gly	Asn	Val	Gly	Phe	Thr	Gly	
123				260					265					270			
124	Gly	Ile	Asn	Ser	Ala	Ile	Leu	Arg	Tyr	Asp	Gly	Ala	Ala	Ala	Val	Glu	
125			275					280					285				
126	Pro	Thr	Thr	Thr	Gln	Thr	Thr	Ser	Thr	Ala	Pro	Leu	Asn	Glu	Val	Asn	
127		290					295					300					
128	Leu	His	Pro	Leu	Val	Thr	Thr	Ala	Val	Pro	Gly	Ser	Pro	Val	Ala	Gly	
129	305					310					315					320	
130	Gly	Val	Asp	Leu	Ala	Ile	Asn	Met	Ala	Phe	Asn	Phe	Asn	Gly	Thr	Asn	
131					325					330					335		
132	Phe	Phe	Ile	Asn	Gly	Ala	Ser	Phe	Thr	Pro	Pro	Thr	Val	Pro	Val	Leu	
133				340					345					350			

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144   Ala Gly Asp Asn Val Thr Ile Arg Phe Arg Thr Asp Asn Pro Gly Pro
145           435                     440                     445
146   Trp Phe Leu His Cys His Ile Asp Phe His Leu Glu Ala Gly Phe Ala
147           450                     455                     460
148   Val Val Phe Ala Glu Asp Ile Pro Asp Val Ala Ser Ala Asn Pro Val
149   465                     470                     475                     480
150   Pro Gln Ala Trp Ser Asp Leu Cys Pro Thr Tyr Asp Ala Leu Asp Pro
151           485                     490                     495
152   Ser Asp Gln
154 <210> SEQ ID NO: 3
155 <211> LENGTH: 499
156 <212> TYPE: PRT
157 <213> ORGANISM: Polyporus pinsitus
158 <400> SEQUENCE: 3
159   Ala Ile Gly Pro Val Ala Ser Leu Val Val Ala Asn Ala Pro Val Ser
160   1           5           10           15
161   Pro Asp Gly Phe Leu Arg Asp Ala Ile Val Val Asn Gly Val Val Pro
162           20           25           30
163   Ser Pro Leu Ile Thr Gly Lys Lys Gly Asp Arg Phe Gln Leu Asn Val
164           35           40           45
165   Val Asp Thr Leu Thr Asn His Ser Met Leu Lys Ser Thr Ser Ile His
166   50           55           60
167   Trp His Gly Phe Phe Gln Ala Gly Thr Asn Trp Ala Glu Gly Pro Ala
168   65           70           75           80
169   Phe Val Asn Gln Cys Pro Ile Ala Ser Gly His Ser Phe Leu Tyr Asp
170           85           90           95
171   Phe His Val Pro Asp Gln Ala Gly Thr Phe Trp Tyr His Ser His Leu
172           100          105          110
173   Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Phe Val Val Tyr Asp
174           115          120          125
175   Pro Lys Asp Pro His Ala Ser Arg Tyr Asp Val Asp Asn Glu Ser Thr
176           130          135          140
177   Val Ile Thr Leu Thr Asp Trp Tyr His Thr Ala Ala Arg Leu Gly Pro
178   145          150          155          160
179   Lys Phe Pro Leu Gly Ala Asp Ala Thr Leu Ile Asn Gly Leu Gly Arg
180           165          170          175
181   Ser Ala Ser Thr Pro Thr Ala Ala Leu Ala Val Ile Asn Val Gln His
182           180          185          190
183   Gly Lys Arg Tyr Arg Phe Arg Leu Val Ser Ile Ser Cys Asp Pro Asn
184           195          200          205
185   Tyr Thr Phe Ser Ile Asp Gly His Asn Leu Thr Val Ile Glu Val Asp
186           210          215          220
187   Gly Ile Asn Ser Gln Pro Leu Leu Val Asp Ser Ile Gln Ile Phe Ala
188   225          230          235          240
189   Ala Gln Arg Tyr Ser Phe Val Leu Asn Ala Asn Gln Thr Val Gly Asn
190           245          250          255
191   Tyr Trp Val Arg Ala Asn Pro Asn Phe Gly Thr Val Gly Phe Ala Gly
192           260          265          270
193   Gly Ile Asn Ser Ala Ile Leu Arg Tyr Gln Gly Ala Pro Val Ala Glu

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194          275          280          285
195  Pro Thr Thr Thr Gln Thr Pro Ser Val Ile Pro Leu Ile Glu Thr Asn
196          290          295          300
197  Leu His Pro Leu Ala Arg Met Pro Val Pro Gly Ser Pro Thr Pro Gly
198  305          310          315          320
199  Gly Val Asp Lys Ala Leu Asn Leu Ala Phe Asn Phe Asn Gly Thr Asn
200          325          330          335
201  Phe Phe Ile Asn Asn Ala Thr Phe Thr Pro Pro Thr Val Pro Val Leu
202          340          345          350
203  Leu Gln Ile Leu Ser Gly Ala Gln Thr Ala Gln Asp Leu Leu Pro Ala
204          355          360          365
205  Gly Ser Val Tyr Pro Leu Pro Ala His Ser Thr Ile Glu Ile Thr Leu
206          370          375          380
207  Pro Ala Thr Ala Leu Ala Pro Gly Ala Pro His Pro Phe His Leu His
208  385          390          395          400
209  Gly His Ala Phe Ala Val Val Arg Ser Ala Gly Ser Thr Thr Tyr Asn
210          405          410          415
211  Tyr Asn Asp Pro Ile Phe Arg Asp Val Val Ser Thr Gly Thr Pro Ala
212          420          425          430
213  Ala Gly Asp Asn Val Thr Ile Arg Phe Gln Thr Asp Asn Pro Gly Pro
214          435          440          445
215  Trp Phe Leu His Cys His Ile Asp Phe His Leu Asp Ala Gly Phe Ala
216          450          455          460
217  Ile Val Phe Ala Glu Asp Val Ala Asp Val Lys Ala Ala Asn Pro Val
218  465          470          475          480
219  Pro Lys Ala Trp Ser Asp Leu Cys Pro Ile Tyr Asp Gly Leu Ser Glu
220          485          490          495
221  Ala Asn Gln
223 <210> SEQ ID NO: 4
224 <211> LENGTH: 548
225 <212> TYPE: PRT
226 <213> ORGANISM: Phlebia radiata
227 <400> SEQUENCE: 4
228  Met His Thr Phe Leu Arg Ser Thr Ala Leu Val Val Ala Gly Leu Ser
229  1          5          10          15
230  Ala Arg Ala Leu Ala Ser Ile Gly Pro Val Thr Asp Phe His Ile Val
231          20          25          30
232  Asn Ala Ala Val Ser Pro Asp Gly Phe Ser Arg Gln Ala Val Leu Ala
233          35          40          45
234  Glu Gly Val Phe Pro Gly Pro Leu Ile Ala Gly Asn Lys Gly Asp Asn
235          50          55          60
236  Phe Gln Ile Asn Val Ile Asp Glu Leu Thr Asn Ala Thr Met Leu Lys
237  65          70          75          80
238  Thr Thr Thr Ile His Trp His Gly Phe Phe Gln His Gly Thr Asn Trp
239          85          90          95
240  Ala Asp Gly Pro Ala Phe Ile Asn Gln Cys Pro Ile Ala Ser Gly Asp
241          100          105          110
242  Ser Phe Leu Tyr Asn Phe Gln Val Pro Asp Gln Ala Gly Thr Phe Trp
243          115          120          125

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/869,877

DATE: 05/08/2002
TIME: 11:03:36

Input Set : N:\paola\US09869877.raw
Output Set: N:\CRF3\05082002\I869877.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 218,234,557

VERIFICATION SUMMARY

DATE: 05/08/2002

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Input Set : N:\paola\US09869877.raw

Output Set: N:\CRF3\05082002\I869877.raw

L:621 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:624 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:651 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:208
L:653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:224
L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:544